IFWO

RAW SEQUENCE LISTING   DATE: 08/09/2004
PATENT APPLICATION: **US/10/679,580A**   TIME: 10:30:59

Input Set : **A:\224378.ST25.txt**
Output Set: **N:\CRF4\08092004\J679580A.raw**

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 3 <110> APPLICANT: Usha KASID
 4        Deepak KUMAR
 5        Irman AHMAD
 7 <120> TITLE OF INVENTION: GENE SCC-112 AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
 9 <130> FILE REFERENCE: 224378
W--> 10 <140> CURRENT APPLICATION NUMBER: US/10/679,580A
11 <141> CURRENT FILING DATE: 2003-10-06
12 <150> PRIOR APPLICATION NUMBER: PCT/US02/10850
13 <151> PRIOR FILING DATE: 2002-04-08
15 <150> PRIOR APPLICATION NUMBER: 60/281,780
16 <151> PRIOR FILING DATE: 2001-04-06
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: PatentIn Ver. 3.2
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 6744
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (232)..(4122)
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36 gcgtgcgggc gggccgcggg ggtcccggac ggacacaagc gcacacactc ccggaagatc 180
38 gcttaccctc cggggtaaa agagatcacc gacaagatca ccacggacga g atg atc 237
39                                                          Met Ile
40                                                            1
42 aaa cgc ctg aag atg gta gtg aaa acc ttt atg gat atg gat cag gac 285
43 Lys Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
44         5                   10                  15
46 tca gaa gat gaa aaa cag cag tat ctc cca cta gcc ttg cat ctt gca 333
47 Ser Glu Asp Glu Lys Gln Gln Tyr Leu Pro Leu Ala Leu His Leu Ala
48         20                  25                  30
50 tct gaa ttc ttc ctc agg aac ccc aat aaa gat gtg cgt ctc ctt gta 381
51 Ser Glu Phe Phe Leu Arg Asn Pro Asn Lys Asp Val Arg Leu Leu Val
52   35                  40                  45                  50
54 gca tgt tgt ttg gct gat atc ttt cgt atc tat gcc cca gaa gct cca 429
55 Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
56                 55                  60                  65
58 tat act tcc cat gat aaa ctt aag gac ata ttt ttg ttt att acc aga 477
59 Tyr Thr Ser His Asp Lys Leu Lys Asp Ile Phe Leu Phe Ile Thr Arg
60                 70                  75                  80
62 caa tta aaa ggt ttg gag gat aca aag agt cca cag ttt aat aga tac 525
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63 Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg Tyr
64          85                   90                  95
66 ttt tat tta tta gag aat tta gct tgg gtt aaa tca tat aac atc tgc   573
67 Phe Tyr Leu Leu Glu Asn Leu Ala Trp Val Lys Ser Tyr Asn Ile Cys
68      100                 105                 110
70 ttt gaa ttg gaa gat tgc aat gaa att ttt att cag ctt ttt aga act   621
71 Phe Glu Leu Glu Asp Cys Asn Glu Ile Phe Ile Gln Leu Phe Arg Thr
72 115                 120                 125                 130
74 ctc ttc tca gtg atc aac aat agc cac aat aag aag gta caa atg cac   669
75 Leu Phe Ser Val Ile Asn Asn Ser His Asn Lys Lys Val Gln Met His
76              135                 140                 145
78 atg cta gat ttg atg agt tct atc atc atg gaa ggt gat gga gtt act   717
79 Met Leu Asp Leu Met Ser Ser Ile Ile Met Glu Gly Asp Gly Val Thr
80          150                 155                 160
82 caa gaa tta ttg ggc tcc att ctt att aac ctc att cct gca cat aag   765
83 Gln Glu Leu Leu Gly Ser Ile Leu Ile Asn Leu Ile Pro Ala His Lys
84          165                 170                 175
86 aac tta aat aaa cag tcc ttt gac ctt gca aaa gtg cta ttg aaa aga   813
87 Asn Leu Asn Lys Gln Ser Phe Asp Leu Ala Lys Val Leu Leu Lys Arg
88      180                 185                 190
90 aca gtc cag act att gag gca tgc att gcc aat ttt ttc aat caa gtc   861
91 Thr Val Gln Thr Ile Glu Ala Cys Ile Ala Asn Phe Phe Asn Gln Val
92 195                 200                 205                 210
94 ctg gtg ctg gga aga tca tca gta agt gat ttg tca gaa cat gta ttt   909
95 Leu Val Leu Gly Arg Ser Ser Val Ser Asp Leu Ser Glu His Val Phe
96              215                 220                 225
98 gat ctg att cag gaa ctt ttt gct ata gat cct cat tta tta tta tcc   957
99 Asp Leu Ile Gln Glu Leu Phe Ala Ile Asp Pro His Leu Leu Leu Ser
100             230                 235                 240
102 gtc atg cca cag ctt gaa ttc aaa cta aag agc aat gat gga gaa gag  1005
103 Val Met Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Gly Glu Glu
104          245                 250                 255
106 cga tta gct gtt gtt cga ctt cta gct aaa ttg ttt ggc tcc aaa gat  1053
107 Arg Leu Ala Val Val Arg Leu Leu Ala Lys Leu Phe Gly Ser Lys Asp
108      260                 265                 270
110 tct gat ttg gca aca cag aat cgt cct ctt tgg caa tgt ttt ctt gga  1101
111 Ser Asp Leu Ala Thr Gln Asn Arg Pro Leu Trp Gln Cys Phe Leu Gly
112 275                 280                 285                 290
114 cga ttt aat gat att cat gtt cct gtg aga tta gaa agt gtg aaa ttt  1149
115 Arg Phe Asn Asp Ile His Val Pro Val Arg Leu Glu Ser Val Lys Phe
116              295                 300                 305
118 gcc agt cat tgt tta atg aat cac cca gat tta gcg aag gat ctc aca  1197
119 Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu Thr
120              310                 315                 320
122 gaa tat tta aag gtt aga tca cat gat cca gaa gaa gct att cgt cat  1245
123 Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg His
124          325                 330                 335
126 gat gtc att gtt act ata ata aca gct gcc aag agg gac ctg gcc tta  1293
127 Asp Val Ile Val Thr Ile Ile Thr Ala Ala Lys Arg Asp Leu Ala Leu
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128      340                   345                   350
130 gta aat gat cag ctg ctt ggc ttt gta agg gaa aga aca ctg gat aaa   1341
131 Val Asn Asp Gln Leu Leu Gly Phe Val Arg Glu Arg Thr Leu Asp Lys
132 355                   360                   365                   370
134 cgg tgg cga gta aga aaa gaa gct atg atg ggt ctg gct cag ctt tat   1389
135 Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Leu Tyr
136                   375                   380                   385
138 aag aaa tac tgt ctt cat ggt gaa gca gga aag gaa gct gca gag aaa   1437
139 Lys Lys Tyr Cys Leu His Gly Glu Ala Gly Lys Glu Ala Ala Glu Lys
140                   390                   395                   400
142 gtc agc tgg ata aag gac aaa ctt ctg cat att tat tat cag aac agc   1485
143 Val Ser Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn Ser
144           405                   410                   415
146 att gac gac aaa ctg ttg gta gag aaa atc ttt gct cag tat ctt gtc   1533
147 Ile Asp Asp Lys Leu Leu Val Glu Lys Ile Phe Ala Gln Tyr Leu Val
148           420                   425                   430
150 ccc cac aac ctg gaa aca gaa gag aga atg aaa tgc tta tat tac tta   1581
151 Pro His Asn Leu Glu Thr Glu Glu Arg Met Lys Cys Leu Tyr Tyr Leu
152 435                   440                   445                   450
154 tat gct agt ttg gat cca aat gct gta aaa gct ctc aac gaa atg tgg   1629
155 Tyr Ala Ser Leu Asp Pro Asn Ala Val Lys Ala Leu Asn Glu Met Trp
156                   455                   460                   465
158 aag tgt cag aac atg ctt cgg agc cat gta cgc gaa cta ttg gat ttg   1677
159 Lys Cys Gln Asn Met Leu Arg Ser His Val Arg Glu Leu Leu Asp Leu
160           470                   475                   480
162 cac aag cag cct aca tca gag gct aac tgt tct gcc atg ttt gga aaa   1725
163 His Lys Gln Pro Thr Ser Glu Ala Asn Cys Ser Ala Met Phe Gly Lys
164           485                   490                   495
166 ctg atg acc ata gca aag aat ttg cct gac ccc ggg aaa gca caa gat   1773
167 Leu Met Thr Ile Ala Lys Asn Leu Pro Asp Pro Gly Lys Ala Gln Asp
168           500                   505                   510
170 ttt gtg aag aaa ttt aac cag gtt ctc ggc gat gat gag aaa ctt cgg   1821
171 Phe Val Lys Lys Phe Asn Gln Val Leu Gly Asp Asp Glu Lys Leu Arg
172 515                   520                   525                   530
174 tct cag ttg gag tta tta att agc cca acc tgt tct tgc aaa caa gca   1869
175 Ser Gln Leu Glu Leu Leu Ile Ser Pro Thr Cys Ser Cys Lys Gln Ala
176                   535                   540                   545
178 gat att tgt gtg aga gaa ata gcc cgg aaa ctt gca aat cct aag caa   1917
179 Asp Ile Cys Val Arg Glu Ile Ala Arg Lys Leu Ala Asn Pro Lys Gln
180           550                   555                   560
182 cca aca aat cct ttt cta gag atg gtc aaa ttt ctg ttg gaa aga atc   1965
183 Pro Thr Asn Pro Phe Leu Glu Met Val Lys Phe Leu Leu Glu Arg Ile
184           565                   570                   575
186 gca cct gtg cac att gat tca gaa gcc ata agt gca cta gtg aaa ttg   2013
187 Ala Pro Val His Ile Asp Ser Glu Ala Ile Ser Ala Leu Val Lys Leu
188           580                   585                   590
190 atg aat aag tca ata gag ggg aca gca gat gat gaa gag gag ggt gta   2061
191 Met Asn Lys Ser Ile Glu Gly Thr Ala Asp Asp Glu Glu Glu Gly Val
192 595                   600                   605                   610
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194 agt cca gat aca gct atc cgt tca gga ctt gaa ctt ctt aag gtt ctg   2109
195 Ser Pro Asp Thr Ala Ile Arg Ser Gly Leu Glu Leu Leu Lys Val Leu
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198 tct ttt aca cat cct acc tcg ttc cac tct gca gag aca tat gag tcc   2157
199 Ser Phe Thr His Pro Thr Ser Phe His Ser Ala Glu Thr Tyr Glu Ser
200             630               635                640
202 ttg tta cag tgc cta aga atg gag gat gac aag gta gca gaa gct gct   2205
203 Leu Leu Gln Cys Leu Arg Met Glu Asp Asp Lys Val Ala Glu Ala Ala
204             645               650                655
206 att caa att ttt aga aat aca ggt cac aaa ata gaa aca gac ctt ccc   2253
207 Ile Gln Ile Phe Arg Asn Thr Gly His Lys Ile Glu Thr Asp Leu Pro
208      660               665                670
210 cag ata cga tcg acc tta att ccc att tta cat caa aaa gca aag agg   2301
211 Gln Ile Arg Ser Thr Leu Ile Pro Ile Leu His Gln Lys Ala Lys Arg
212 675               680                685                690
214 ggt act cca cac caa gca aaa cag gct gtg cac tgt ata cac gcc ata   2349
215 Gly Thr Pro His Gln Ala Lys Gln Ala Val His Cys Ile His Ala Ile
216             695               700         ·      705
218 ttc aca aat aaa gaa gtc cag ctt gca cag att ttt gag cca ctc agt   2397
219 Phe Thr Asn Lys Glu Val Gln Leu Ala Gln Ile Phe Glu Pro Leu Ser
220             710               715                720
222 agg agt ctg aat gct gat gtg cca gaa caa ctt ata act cca tta gtt   2445
223 Arg Ser Leu Asn Ala Asp Val Pro Glu Gln Leu Ile Thr Pro Leu Val
224             725               730                735
226 tca ttg ggc cac att tct atg tta gca cca gat cag ttt gct tcc cca   2493
227 Ser Leu Gly His Ile Ser Met Leu Ala Pro Asp Gln Phe Ala Ser Pro
228      740               745                750
230 atg aaa tct gta gta gca aat ttt att gtg aaa gat ctg cta atg aat   2541
231 Met Lys Ser Val Val Ala Asn Phe Ile Val Lys Asp Leu Leu Met Asn
232 755               760                765                770
234 gac agg tca aca ggt gaa aag aat gga aaa ctg tgg tct cca gat gaa   2589
235 Asp Arg Ser Thr Gly Glu Lys Asn Gly Lys Leu Trp Ser Pro Asp Glu
236             775               780                785
238 gag gtt tcc cct gaa gta cta gca aag gta cag gca att aaa ctt ctg   2637
239 Glu Val Ser Pro Glu Val Leu Ala Lys Val Gln Ala Ile Lys Leu Leu
240             790         ·      795         ·      800   ·
242 gta agg tgg ctg ttg ggt atg aaa aac aac cag tct aaa tct gcc aat   2685
243 Val Arg Trp Leu Leu Gly Met Lys Asn Asn Gln Ser Lys Ser Ala Asn
244             805               810                815
246 tca acc ctt cgg tta tta tca gcg atg ttg gtt agt gag ggt gac ctg   2733
247 Ser Thr Leu Arg Leu Leu Ser Ala Met Leu Val Ser Glu Gly Asp Leu
248      820               825                830
250 aca gag caa aag agg atc agt aaa tct gat atg tct cgc ttg cga tta   2781
251 Thr Glu Gln Lys Arg Ile Ser Lys Ser Asp Met Ser Arg Leu Arg Leu
252 835               840                845                850
254 gct gct ggt agt gcc ata atg aag ctt gct cag gaa cct tgt tac cat   2829
255 Ala Ala Gly Ser Ala Ile Met Lys Leu Ala Gln Glu Pro Cys Tyr His
256             855               860                865
258 gaa att att acc cca gaa cag ttt cag ctc tgt gca ctt gtt att aat   2877
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259 Glu Ile Ile Thr Pro Glu Gln Phe Gln Leu Cys Ala Leu Val Ile Asn
260              870               875               880
262 gat gag tgt tac caa gta agg cag ata ttt gct cag aag ctg cat aag  2925
263 Asp Glu Cys Tyr Gln Val Arg Gln Ile Phe Ala Gln Lys Leu His Lys
264       885               890               895
266 gca ctt gtg aag tta ctg ctc cca ttg gag tat atg gcg atc ttt gcc  2973
267 Ala Leu Val Lys Leu Leu Leu Pro Leu Glu Tyr Met Ala Ile Phe Ala
268       900               905               910
270 ttg tgt gcc aaa gat cct gtg aag gag aga aga gca cac gca cga caa  3021
271 Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg Gln
272 915               920               925               930
274 tgt tta ctg aaa aat atc agt ata cgc agg gaa tac att aag cag aat  3069
275 Cys Leu Leu Lys Asn Ile Ser Ile Arg Arg Glu Tyr Ile Lys Gln Asn
276              935               940               945
278 cct atg gct act gag aaa tta tta tca ctg ttg cct gaa tat gta gtt  3117
279 Pro Met Ala Thr Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val Val
280              950               955               960
282 cca tac atg att cac ctg cta gcc cat gat cca gat ttt aca aga tca  3165
283 Pro Tyr Met Ile His Leu Leu Ala His Asp Pro Asp Phe Thr Arg Ser
284       965               970               975
286 caa gat gtt gat cag ctt cgt gat atc aaa gag tgc cta tgg ttc atg  3213
287 Gln Asp Val Asp Gln Leu Arg Asp Ile Lys Glu Cys Leu Trp Phe Met
288       980               985               990
290 ctt gaa gtt tta atg aca aag aat gaa aac aat agc cat gcc ttt atg  3261
291 Leu Glu Val Leu Met Thr Lys Asn Glu Asn Asn Ser His Ala Phe Met
292 995               1000              1005              1010
294 aag aag atg gca gag aac atc aag tta acc aga gat gcc cag tct cca  3309
295 Lys Lys Met Ala Glu Asn Ile Lys Leu Thr Arg Asp Ala Gln Ser Pro
296              1015              1020              1025
298 gat gaa tcc aag aca aat gaa aaa ctg tat aca gta tgt gat gtg gct  3357
299 Asp Glu Ser Lys Thr Asn Glu Lys Leu Tyr Thr Val Cys Asp Val Ala
300              1030              1035              1040
302 ctc tgt gtt ata aat agt aaa agt gct ttg tgc aat gca gat tca cca  3405
303 Leu Cys Val Ile Asn Ser Lys Ser Ala Leu Cys Asn Ala Asp Ser Pro
304       1045              1050              1055
306 aag gac cca gtc ctc cca atg aaa ttt ttt aca caa cct gaa aag gac  3453
307 Lys Asp Pro Val Leu Pro Met Lys Phe Phe Thr Gln Pro Glu Lys Asp
308    1060              1065              1070
310 ttc tgt aac gat aag agt tat att tca gaa gag aca aga gta ctt ctg  3501
311 Phe Cys Asn Asp Lys Ser Tyr Ile Ser Glu Glu Thr Arg Val Leu Leu
312 1075              1080              1085              1090
314 tta aca gga aag cca aag cct gct gga gta cta ggt gca gta aat aag  3549
315 Leu Thr Gly Lys Pro Lys Pro Ala Gly Val Leu Gly Ala Val Asn Lys
316              1095              1100              1105
318 cct tta tca gca acg gga agg aaa ccc tat gtt aga agc act ggc act  3597
319 Pro Leu Ser Ala Thr Gly Arg Lys Pro Tyr Val Arg Ser Thr Gly Thr
320              1110              1115              1120
322 gag act gga agc aat att aat gta aat tca gag ctg aac cct tca acc  3645
323 Glu Thr Gly Ser Asn Ile Asn Val Asn Ser Glu Leu Asn Pro Ser Thr
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Input Set : **A:\224378.ST25.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3

VERIFICATION SUMMARY   DATE: 08/09/2004
PATENT APPLICATION: **US/10/679,580A**   TIME: 10:31:00

Input Set : **A:\224378.ST25.txt**
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